SEQUENCE LISTING

<110> Susan M. Freier
     Brenda F. Baker
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<120> ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING PROTEIN-1
EXPRESSION

<130> ISIS0046-500

<150> US 10/161996

<151> 2002/06/04

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acgaggcggc gggcccggcg ggcctcccgg aggaggcggc tgcgcc atg gac gag      175
                                                   Met Asp Glu
                                                    1

cca ccc ttc agc gag gcg gct ttg gag cag gcg ctg ggc gag ccg tgc    223
Pro Pro Phe Ser Glu Ala Ala Leu Glu Gln Ala Leu Gly Glu Pro Cys
     5                  10                  15

gat ctg gac gcg gcg ctg ctg acc gac atc gaa gac atg ctt cag ctt    271
Asp Leu Asp Ala Ala Leu Leu Thr Asp Ile Glu Asp Met Leu Gln Leu
 20                  25                  30                  35

atc aac aac caa gac agt gac ttc cct ggc cta ttt gac cca ccc tat    319
Ile Asn Asn Gln Asp Ser Asp Phe Pro Gly Leu Phe Asp Pro Pro Tyr
                 40                  45                  50

gct ggg agt ggg gca ggg ggc aca gac cct gcc agc ccc gat acc agc    367
Ala Gly Ser Gly Ala Gly Gly Thr Asp Pro Ala Ser Pro Asp Thr Ser
             55                  60                  65

tcc cca ggc agc ttg tct cca cct cct gcc aca ttg agc tcc tct ctt    415
Ser Pro Gly Ser Leu Ser Pro Pro Pro Ala Thr Leu Ser Ser Ser Leu
             70                  75                  80

gaa gcc ttc ctg agc ggg ccg cag gca gcg ccc tca ccc ctg tcc cct    463
Glu Ala Phe Leu Ser Gly Pro Gln Ala Ala Pro Ser Pro Leu Ser Pro
     85                  90                  95

ccc cag cct gca ccc act cca ttg aag atg tac ccg tcc atg ccc gct    511
Pro Gln Pro Ala Pro Thr Pro Leu Lys Met Tyr Pro Ser Met Pro Ala
100                 105                 110                 115

ttc tcc cct ggg cct ggt atc aag gaa gag tca gtg cca ctg agc atc    559
Phe Ser Pro Gly Pro Gly Ile Lys Glu Glu Ser Val Pro Leu Ser Ile
                 120                 125                 130

ctg cag acc ccc acc cca cag ccc ctg cca ggg gcc ctc ctg cca cag    607
Leu Gln Thr Pro Thr Pro Gln Pro Leu Pro Gly Ala Leu Leu Pro Gln
             135                 140                 145

agc ttc cca gcc cca gcc cca ccg cag ttc agc tcc acc cct gtg tta    655
Ser Phe Pro Ala Pro Ala Pro Pro Gln Phe Ser Ser Thr Pro Val Leu
             150                 155                 160

ggc tac ccc agc cct ccg gga ggc ttc tct aca gga agc cct ccc ggg    703
Gly Tyr Pro Ser Pro Pro Gly Gly Phe Ser Thr Gly Ser Pro Pro Gly
             165                 170                 175

aac acc cag cag ccg ctg cct ggc ctg cca ctg gct tcc ccg cca ggg    751
Asn Thr Gln Gln Pro Leu Pro Gly Leu Pro Leu Ala Ser Pro Pro Gly
180                 185                 190                 195

gtc ccg ccc gtc tcc ttg cac acc cag gtc cag agt gtg gtc ccc cag    799
Val Pro Pro Val Ser Leu His Thr Gln Val Gln Ser Val Val Pro Gln
                 200                 205                 210
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cag cta ctg aca gtc aca gct gcc ccc acg gca gcc cct gta acg acc   847
Gln Leu Leu Thr Val Thr Ala Ala Pro Thr Ala Ala Pro Val Thr Thr
            215   220   225

act gtg acc tcg cag atc cag cag gtc ccg gtc ctg ctg cag ccc cac   895
Thr Val Thr Ser Gln Ile Gln Gln Val Pro Val Leu Leu Gln Pro His
            230   235   240

ttc atc aag gca gac tcg ctg ctt ctg aca gcc atg aag aca gac gga   943
Phe Ile Lys Ala Asp Ser Leu Leu Leu Thr Ala Met Lys Thr Asp Gly
            245   250   255

gcc act gtg aag gcg gca ggt ctc agt ccc ctg gtc tct ggc acc act   991
Ala Thr Val Lys Ala Ala Gly Leu Ser Pro Leu Val Ser Gly Thr Thr
260   265   270   275

gtg cag aca ggg cct ttg ccg acc ctg gtg agt ggc gga acc atc ttg   1039
Val Gln Thr Gly Pro Leu Pro Thr Leu Val Ser Gly Gly Thr Ile Leu
            280   285   290

gca aca gtc cca ctg gtc gta gat gcg gag aag ctg cct atc aac cgg   1087
Ala Thr Val Pro Leu Val Val Asp Ala Glu Lys Leu Pro Ile Asn Arg
            295   300   305

ctc gca gct ggc agc aag gcc ccg gcc tct gcc cag agc cgt gga gag   1135
Leu Ala Ala Gly Ser Lys Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu
            310   315   320

aag cgc aca gcc cac aac gcc att gag aag cgc tac cgc tcc tcc atc   1183
Lys Arg Thr Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile
            325   330   335

aat gac aaa atc att gag ctc aag gat ctg gtg gtg ggc act gag gca   1231
Asn Asp Lys Ile Ile Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala
340   345   350   355

aag ctg aat aaa tct gct gtc ttg cgc aag gcc atc gac tac att cgc   1279
Lys Leu Asn Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg
            360   365   370

ttt ctg caa cac agc aac cag aaa ctc aag cag gag aac cta agt ctg   1327
Phe Leu Gln His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu
            375   380   385

cgc act gct gtc cac aaa agc aaa tct ctg aag gat ctg gtg tcg gcc   1375
Arg Thr Ala Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala
            390   395   400

tgt ggc agt gga ggg aac aca gac gtg ctc atg gag ggc gtg aag act   1423
Cys Gly Ser Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr
405   410   415

gag gtg gag gac aca ctg acc cca ccc ccc tcg gat gct ggc tca cct   1471
Glu Val Glu Asp Thr Leu Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro
420   425   430   435

ttc cag agc agc ccc ttg tcc ctt ggc agc agg ggc agt ggc agc ggt   1519
Phe Gln Ser Ser Pro Leu Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly
                440   445   450

ggc agt ggc agt gac tcg gag cct gac agc cca gtc ttt gag gac agc   1567
Gly Ser Gly Ser Asp Ser Glu Pro Asp Ser Pro Val Phe Glu Asp Ser
            455   460   465

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aag gca aag cca gag cag cgg ccg tct ctg cac agc cgg ggc atg ctg        1615
Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg Gly Met Leu
        470             475             480

gac cgc tcc cgc ctg gcc ctg tgc acg ctc gtc ttc ctc tgc ctg tcc        1663
Asp Arg Ser Arg Leu Ala Leu Cys Thr Leu Val Phe Leu Cys Leu Ser
        485             490             495

tgc aac ccc ttg gcc tcc ttg ctg ggg gcc cgg ggg ctt ccc agc ccc        1711
Cys Asn Pro Leu Ala Ser Leu Leu Gly Ala Arg Gly Leu Pro Ser Pro
500             505             510             515

tca gat acc acc agc gtc tac cat agc cct ggg cgc aac gtg ctg ggc        1759
Ser Asp Thr Thr Ser Val Tyr His Ser Pro Gly Arg Asn Val Leu Gly
            520             525             530

acc gag agc aga gat ggc cct ggc tgg gcc cag tgg ctg ctg ccc cca        1807
Thr Glu Ser Arg Asp Gly Pro Gly Trp Ala Gln Trp Leu Leu Pro Pro
            535             540             545

gtg gtc tgg ctg ctc aat ggg ctg ttg gtg ctc gtc tcc ttg gtg ctt        1855
Val Val Trp Leu Leu Asn Gly Leu Leu Val Leu Val Ser Leu Val Leu
        550             555             560

ctc ttt gtc tac ggt gag cca gtc aca cgg ccc cac tca ggc ccc gcc        1903
Leu Phe Val Tyr Gly Glu Pro Val Thr Arg Pro His Ser Gly Pro Ala
        565             570             575

gtg tac ttc tgg agg cat cgc aag cag gct gac ctg gac ctg gcc cgg        1951
Val Tyr Phe Trp Arg His Arg Lys Gln Ala Asp Leu Asp Leu Ala Arg
580             585             590             595

gga gac ttt gcc cag gct gcc cag cag ctg tgg ctg gcc ctg cgg gca        1999
Gly Asp Phe Ala Gln Ala Ala Gln Gln Leu Trp Leu Ala Leu Arg Ala
            600             605             610

ctg ggc cgg ccc ctg ccc acc tcc cac ctg gac ctg gct tgt agc ctc        2047
Leu Gly Arg Pro Leu Pro Thr Ser His Leu Asp Leu Ala Cys Ser Leu
            615             620             625

ctc tgg aac ctc atc cgt cac ctg ctg cag cgt ctc tgg gtg ggc cgc        2095
Leu Trp Asn Leu Ile Arg His Leu Leu Gln Arg Leu Trp Val Gly Arg
            630             635             640

tgg ctg gca ggc cgg gca ggg ggc ctg cag cag gac tgt gct ctg cga        2143
Trp Leu Ala Gly Arg Ala Gly Gly Leu Gln Gln Asp Cys Ala Leu Arg
        645             650             655

gtg gat gct agc gcc agc gcc cga gac gca gcc ctg gtc tac cat aag        2191
Val Asp Ala Ser Ala Ser Ala Arg Asp Ala Ala Leu Val Tyr His Lys
660             665             670             675

ctg cac cag ctg cac acc atg ggg aag cac aca ggc ggg cac ctc act        2239
Leu His Gln Leu His Thr Met Gly Lys His Thr Gly Gly His Leu Thr
            680             685             690

gcc acc aac ctg gcg ctg agt gcc ctg aac ctg gca gag tgt gca ggg        2287
Ala Thr Asn Leu Ala Leu Ser Ala Leu Asn Leu Ala Glu Cys Ala Gly
            695             700             705

gat gcc gtg tct gtg gcg acg ctg gcc gag atc tat gtg gcg gct gca        2335
Asp Ala Val Ser Val Ala Thr Leu Ala Glu Ile Tyr Val Ala Ala Ala
        710             715             720
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ttg aga gtg aag acc agt ctc cca cgg gcc ttg cat ttt ctg aca cgc   2383
Leu Arg Val Lys Thr Ser Leu Pro Arg Ala Leu His Phe Leu Thr Arg
    725             730              735

ttc ttc ctg agc agt gcc cgc cag gcc tgc ctg gca cag agt ggc tca   2431
Phe Phe Leu Ser Ser Ala Arg Gln Ala Cys Leu Ala Gln Ser Gly Ser
740             745              750              755

gtg cct cct gcc atg cag tgg ctc tgc cac ccc gtg ggc cac cgt ttc   2479
Val Pro Pro Ala Met Gln Trp Leu Cys His Pro Val Gly His Arg Phe
            760              765              770

ttc gtg gat ggg gac tgg tcc gtg ctc agt acc cca tgg gag agc ctg   2527
Phe Val Asp Gly Asp Trp Ser Val Leu Ser Thr Pro Trp Glu Ser Leu
        775              780              785

tac agc ttg gcc ggg aac cca gtg gac ccc ctg gcc cag gtg act cag   2575
Tyr Ser Leu Ala Gly Asn Pro Val Asp Pro Leu Ala Gln Val Thr Gln
        790              795              800

cta ttc cgg gaa cat ctc tta gag cga gca ctg aac tgt gtg acc cag   2623
Leu Phe Arg Glu His Leu Leu Glu Arg Ala Leu Asn Cys Val Thr Gln
    805              810              815

ccc aac ccc agc cct ggg tca gct gat ggg gac aag gaa ttc tcg gat   2671
Pro Asn Pro Ser Pro Gly Ser Ala Asp Gly Asp Lys Glu Phe Ser Asp
820              825              830              835

gcc ctc ggg tac ctg cag ctg ctg aac agc tgt tct gat gct gcg ggg   2719
Ala Leu Gly Tyr Leu Gln Leu Leu Asn Ser Cys Ser Asp Ala Ala Gly
            840              845              850

gct cct gcc tac agc ttc tcc atc agt tcc agc atg gcc acc acc acc   2767
Ala Pro Ala Tyr Ser Phe Ser Ile Ser Ser Ser Met Ala Thr Thr Thr
            855              860              865

ggc gta gac ccg gtg gcc aag tgg tgg gcc tct ctg aca gct gtg gtg   2815
Gly Val Asp Pro Val Ala Lys Trp Trp Ala Ser Leu Thr Ala Val Val
        870              875              880

atc cac tgg ctg cgg cgg gat gag gag gcg gct gag cgg ctg tgc ccg   2863
Ile His Trp Leu Arg Arg Asp Glu Glu Ala Ala Glu Arg Leu Cys Pro
    885              890              895

ctg gtg gag cac ctg ccc cgg gtg ctg cag gag tct gag aga ccc ctg   2911
Leu Val Glu His Leu Pro Arg Val Leu Gln Glu Ser Glu Arg Pro Leu
900              905              910              915

ccc agg gca gct ctg cac tcc ttc aag gct gcc cgg gcc ctg ctg ggc   2959
Pro Arg Ala Ala Leu His Ser Phe Lys Ala Ala Arg Ala Leu Leu Gly
            920              925              930

tgt gcc aag gca gag tct ggt cca gcc agc ctg acc atc tgt gag aag   3007
Cys Ala Lys Ala Glu Ser Gly Pro Ala Ser Leu Thr Ile Cys Glu Lys
            935              940              945

gcc agt ggg tac ctg cag gac agc ctg gct acc aca cca gcc agc agc   3055
Ala Ser Gly Tyr Leu Gln Asp Ser Leu Ala Thr Thr Pro Ala Ser Ser
        950              955              960

tcc att gac aag gcc gtg cag ctg ttc ctg tgt gac ctg ctt ctt gtg   3103
Ser Ile Asp Lys Ala Val Gln Leu Phe Leu Cys Asp Leu Leu Leu Val
    965              970              975
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gtg cgc acc agc ctg tgg cgg cag cag cag ccc ccg gcc ccg gcc cca    3151
Val Arg Thr Ser Leu Trp Arg Gln Gln Gln Pro Pro Ala Pro Ala Pro
980             985             990             995

gca gcc cag ggc gcc agc agc agg ccc cag gct tcc gcc ctt gag ctg    3199
Ala Ala Gln Gly Ala Ser Ser Arg Pro Gln Ala Ser Ala Leu Glu Leu
                1000            1005            1010

cgt ggc ttc caa cgg gac ctg agc agc ctg agg cgg ctg gca cag agc    3247
Arg Gly Phe Gln Arg Asp Leu Ser Ser Leu Arg Arg Leu Ala Gln Ser
                1015            1020            1025

ttc cgg ccc gcc atg cgg agg gtg ttc cta cat gag gcc acg gcc cgg    3295
Phe Arg Pro Ala Met Arg Arg Val Phe Leu His Glu Ala Thr Ala Arg
        1030            1035            1040

ctg atg gcg ggg gcc agc ccc aca cgg aca cac cag ctc ctc gac cgc    3343
Leu Met Ala Gly Ala Ser Pro Thr Arg Thr His Gln Leu Leu Asp Arg
        1045            1050            1055

agt ctg agg cgg cgg gca ggc ccc ggt ggc aaa gga ggc gcg gtg gcg    3391
Ser Leu Arg Arg Arg Ala Gly Pro Gly Gly Lys Gly Gly Ala Val Ala
1060            1065            1070            1075

gag ctg gag ccg cgg ccc acg cgg cgg gag cac gcg gag gcc ttg ctg    3439
Glu Leu Glu Pro Arg Pro Thr Arg Arg Glu His Ala Glu Ala Leu Leu
                1080            1085            1090

ctg gcc tcc tgc tac ctg ccc ccc ggc ttc ctg tcg gcg ccc ggg cag    3487
Leu Ala Ser Cys Tyr Leu Pro Pro Gly Phe Leu Ser Ala Pro Gly Gln
                1095            1100            1105

cgc gtg ggc atg ctg gct gag gcg gcg cgc aca ctc gag aag ctt ggc    3535
Arg Val Gly Met Leu Ala Glu Ala Ala Arg Thr Leu Glu Lys Leu Gly
        1110            1115            1120

gat cgc cgg ctg ctg cac gac tgt cag cag atg ctc atg cgc ctg ggc    3583
Asp Arg Arg Leu Leu His Asp Cys Gln Gln Met Leu Met Arg Leu Gly
        1125            1130            1135

ggt ggg acc act gtc act tcc agc tag accccgtgtc cccggcctca          3630
Gly Gly Thr Thr Val Thr Ser Ser
1140            1145

gcacccctgt ctctagccac tttggtcccg tgcagcttct gtcctgcgtc gaagctttga  3690

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<223> PCR Probe

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<223> PCR Primer

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cctgggcagc gaatgagcat gctggccgag gcggcacgca ccgtagagaa gcttggcgat      3480

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ggtgctgacc tctggtggcc gatcggggca ctgcaggggc cgagccattt tgggggggccc 25620

ccctccttgc tctgcaggca ccttagtggc ttttttcctc ctgtgtacag ggaagagagg 25680

ggtacatttc cctgtgctga cggaagccaa cttggctttc ccggactgca agcagggctc 25740

tgccccagag gcctctctct ccgtcgtggg agagagacgt gtacatagtg taggtcagcg 25800

tgcttagcct cctgacctga ggctcctgtg ctactttgcc ttttgcaaac tttattttca 25860

tagattgaga agttttgtac agagaattaa aaatgaaatt atttataatc tgggttttgt 25920

gtcttcagct gatggatgtg ctgactagtg agagtgcttg ggccctcccc cagcacctag 25980

ggaaaggctt cccctccccc tccggccaca aggtacacaa cttttaactt agctcttccc 26040

gatgtttgtt tgttagtggg aggagtgggg agggctggct gtatggcctc cagcctacct 26100

gttccccctg ctcccagggc acatggttgg gctgtgtcaa cccttagggc ctccatgggg 26160

tcagttgtcc cttctcacct cccagctctg tccccatcag gtccctgggt ggcacgggag 26220

gatggactga cttccaggac ctgttgtgtg acaggagcta cagcttgggt ctccctgcaa 26280

gaagtctggc acgtctcacc tcccccatcc cggcccctgg tcatctcaca gcaaagaagc 26340

ctcctccctc ccgacctgcc gccacactgg agagggggca caggggcggg ggaggtttcc 26400

tgttctgtga aaggccgact ccctgactcc attcatgccc ccccccccag cccctccctt 26460

cattcccatt ccccaaccta aagcctggcc cggctcccag ctgaatctgg tcggaatcca 26520

cgggctgcag attttccaaa acaatcgttg tatctttatt gactttttt tttttttttt 26580

tctgaatgca atgactgttt tttactctta aggaaaataa acatctttta gaaacagctc 26640

gatacacaca atcttcagtg tgaagcaata tactaataag aacactagtc gtcttaacat 26700

ttacagtctt catatatatt atatatatgt atatgtatac atatatatac actatataac 26760

gaggccagat ataatacaca cgtttaccat tttacagtca tatgtacagg aagttgctag 26820

ggcggccctg ggctgggggc tgcgtcaggc ctatcgaagc gtggacagag ctgaggacac 26880

ggacggacag gcggacggac tggcagggac tggcccgggc cggtggtggc tgcgtggaca 26940

agtggcgtcg cggtagcccc ttacccggca aaggcccggt tggggctctg ttgcgggcgc 27000

a                                                                  27001
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<210> 19
<211> 698
<212> DNA
<213> H. sapiens

<220>

<400> 19
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cgggcgcaga tcgcggagcc atggattgca ctttcgaaga catgcttcag cttatcaaca     120
```

```
accaagacag tgacttccct ggcctatttg acccacccta tgctgggagt gggggcagggg    180

gcacagaccc tgccagcccc gataccagct ccccaggcag ctagtctcca cctcctgcca    240

cattgagctc ctctcttgaa gccttcctga gcgggccgca ggcagcgccc tcacccctgt    300

cccctcccca gcctgcaccc actccattga agatgtaccc gtccatgccc gctttctccc    360

ctgggcctgg tatcaaggaa gagtcagtgc cactgagcat cctgcagacc cccaccccac    420

agcccctgcc aggggccctc ctgccacaga gcttcccagc cccagcccca cctgagttca    480

gctccacccc tgtgttaggc taccccagcc ctcctggagg ctactctaca ggaagccctc    540

ccgggaacac ccagcagccg ctgcctggcc tgccactggc ttccccgaca ggggtcccgc    600

ccgtctcctt gcacacccgg gtccagagtg tggtccccca gtagctactg acagtcacag    660

ctggccccac tgcagcccct tgaacgacca ctgtgact                            698
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<210> 20
<211> 4154
<212> DNA
<213> H. sapiens

<220>

<221> CDS
<222> (167)...(3610)

<400> 20
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gcggagcggc ggcggcgact gagagccggg gccgcggcgg cgctccctag gaagggccgt    120

acgaggcggc gggcccggcg ggcctcccgg aggaggcggc tgcgcc atg gac gag      175
                                                     Met Asp Glu
                                                      1
```

```
cca ccc ttc agc gag gcg gct ttg gag cag gcg ctg ggc gag ccg tgc    223
Pro Pro Phe Ser Glu Ala Ala Leu Glu Gln Ala Leu Gly Glu Pro Cys
         5              10                  15
```

```
gat ctg gac gcg gcg ctg ctg acc gac atc gaa gac atg ctt cag ctt    271
Asp Leu Asp Ala Ala Leu Leu Thr Asp Ile Glu Asp Met Leu Gln Leu
 20              25                  30                  35
```

```
atc aac aac caa gac agt gac ttc cct ggc cta ttt gac cca ccc tat    319
Ile Asn Asn Gln Asp Ser Asp Phe Pro Gly Leu Phe Asp Pro Pro Tyr
             40                  45                  50
```

```
gct ggg agt ggg gca ggg ggc aca gac cct gcc agc ccc gat acc agc    367
Ala Gly Ser Gly Ala Gly Gly Thr Asp Pro Ala Ser Pro Asp Thr Ser
             55                  60                  65
```

```
tcc cca ggc agc ttg tct cca cct cct gcc aca ttg agc tcc tct ctt    415
Ser Pro Gly Ser Leu Ser Pro Pro Pro Ala Thr Leu Ser Ser Ser Leu
         70                  75                  80
```

```
gaa gcc ttc ctg agc ggg ccg cag gca gcg ccc tca ccc ctg tcc cct    463
Glu Ala Phe Leu Ser Gly Pro Gln Ala Ala Pro Ser Pro Leu Ser Pro
 85                  90                  95
```

```
ccc cag cct gca ccc act cca ttg aag atg tac ccg tcc atg ccc gct    511
Pro Gln Pro Ala Pro Thr Pro Leu Lys Met Tyr Pro Ser Met Pro Ala
100             105             110             115

ttc tcc cct ggg cct ggt atc aag gaa gag tca gtg cca ctg agc atc    559
Phe Ser Pro Gly Pro Gly Ile Lys Glu Glu Ser Val Pro Leu Ser Ile
                120             125             130

ctg cag acc ccc acc cca cag ccc ctg cca ggg gcc ctc ctg cca cag    607
Leu Gln Thr Pro Thr Pro Gln Pro Leu Pro Gly Ala Leu Leu Pro Gln
            135             140             145

agc ttc cca gcc cca gcc cca ccg cag ttc agc tcc acc cct gtg tta    655
Ser Phe Pro Ala Pro Ala Pro Pro Gln Phe Ser Ser Thr Pro Val Leu
            150             155             160

ggc tac ccc agc cct ccg gga ggc ttc tct aca gga agc cct ccc ggg    703
Gly Tyr Pro Ser Pro Pro Gly Gly Phe Ser Thr Gly Ser Pro Pro Gly
            165             170             175

aac acc cag cag ccg ctg cct ggc ctg cca ctg gct tcc ccg cca ggg    751
Asn Thr Gln Gln Pro Leu Pro Gly Leu Pro Leu Ala Ser Pro Pro Gly
180             185             190             195

gtc ccg ccc gtc tcc ttg cac acc cag gtc cag agt gtg gtc ccc cag    799
Val Pro Pro Val Ser Leu His Thr Gln Val Gln Ser Val Val Pro Gln
                200             205             210

cag cta ctg aca gtc aca gct gcc ccc acg gca gcc cct gta acg acc    847
Gln Leu Leu Thr Val Thr Ala Ala Pro Thr Ala Ala Pro Val Thr Thr
            215             220             225

act gtg acc tcg cag atc cag cag gtc ccg gtc ctg ctg cag ccc cac    895
Thr Val Thr Ser Gln Ile Gln Gln Val Pro Val Leu Leu Gln Pro His
            230             235             240

ttc atc aag gca gac tcg ctg ctt ctg aca gcc atg aag aca gac gga    943
Phe Ile Lys Ala Asp Ser Leu Leu Leu Thr Ala Met Lys Thr Asp Gly
            245             250             255

gcc act gtg aag gcg gca ggt ctc agt ccc ctg gtc tct ggc acc act    991
Ala Thr Val Lys Ala Ala Gly Leu Ser Pro Leu Val Ser Gly Thr Thr
260             265             270             275

gtg cag aca ggg cct ttg ccg acc ctg gtg agt ggc gga acc atc ttg   1039
Val Gln Thr Gly Pro Leu Pro Thr Leu Val Ser Gly Gly Thr Ile Leu
            280             285             290

gca aca gtc cca ctg gtc gta gat gcg gag aag ctg cct atc aac cgg   1087
Ala Thr Val Pro Leu Val Val Asp Ala Glu Lys Leu Pro Ile Asn Arg
            295             300             305

ctc gca gct ggc agc aag gcc ccg gcc tct gcc cag agc cgt gga gag   1135
Leu Ala Ala Gly Ser Lys Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu
            310             315             320

aag cgc aca gcc cac aac gcc att gag aag cgc tac cgc tcc tcc atc   1183
Lys Arg Thr Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile
            325             330             335

aat gac aaa atc att gag ctc aag gat ctg gtg gtg ggc act gag gca   1231
Asn Asp Lys Ile Ile Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala
340             345             350             355
```

```
aag ctg aat aaa tct gct gtc ttg cgc aag gcc atc gac tac att cgc    1279
Lys Leu Asn Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg
            360             365                 370

ttt ctg caa cac agc aac cag aaa ctc aag cag gag aac cta agt ctg    1327
Phe Leu Gln His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu
            375             380                 385

cgc act gct gtc cac aaa agc aaa tct ctg aag gat ctg gtg tcg gcc    1375
Arg Thr Ala Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala
            390             395                 400

tgt ggc agt gga ggg aac aca gac gtg ctc atg gag ggc gtg aag act    1423
Cys Gly Ser Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr
            405             410                 415

gag gtg gag gac aca ctg acc cca ccc ccc tcg gat gct ggc tca cct    1471
Glu Val Glu Asp Thr Leu Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro
420             425                 430                 435

ttc cag agc agc ccc ttg tcc ctt ggc agc agg ggc agt ggc agc ggt    1519
Phe Gln Ser Ser Pro Leu Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly
                440                 445                 450

ggc agt ggc agt gac tcg gag cct gac agc cca gtc ttt gag gac agc    1567
Gly Ser Gly Ser Asp Ser Glu Pro Asp Ser Pro Val Phe Glu Asp Ser
            455                 460                 465

aag gca aag cca gag cag cgg ccg tct ctg cac agc cgg ggc atg ctg    1615
Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg Gly Met Leu
            470                 475                 480

gac cgc tcc cgc ctg gcc ctg tgc acg ctc gtc ttc ctc tgc ctg tcc    1663
Asp Arg Ser Arg Leu Ala Leu Cys Thr Leu Val Phe Leu Cys Leu Ser
            485                 490                 495

tgc aac ccc ttg gcc tcc ttg ctg ggg gcc cgg ggg ctt ccc agc ccc    1711
Cys Asn Pro Leu Ala Ser Leu Leu Gly Ala Arg Gly Leu Pro Ser Pro
500                 505                 510                 515

tca gat acc acc agc gtc tac cat agc cct ggg cgc aac gtg ctg ggc    1759
Ser Asp Thr Thr Ser Val Tyr His Ser Pro Gly Arg Asn Val Leu Gly
                520             525                 530

acc gag agc aga gat ggc cct ggc tgg gcc cag tgg ctg ctg ccc cca    1807
Thr Glu Ser Arg Asp Gly Pro Gly Trp Ala Gln Trp Leu Leu Pro Pro
            535                 540                 545

gtg gtc tgg ctg ctc aat ggg ctg ttg gtg ctc gtc tcc ttg gtg ctt    1855
Val Val Trp Leu Leu Asn Gly Leu Leu Val Leu Val Ser Leu Val Leu
            550                 555                 560

ctc ttt gtc tac ggt gag cca gtc aca cgg ccc cac tca ggc ccc gcc    1903
Leu Phe Val Tyr Gly Glu Pro Val Thr Arg Pro His Ser Gly Pro Ala
            565                 570                 575

gtg tac ttc tgg agg cat cgc aag cag gct gac ctg gac ctg gcc cgg    1951
Val Tyr Phe Trp Arg His Arg Lys Gln Ala Asp Leu Asp Leu Ala Arg
580             585                 590                 595

gga gac ttt gcc cag gct gcc cag cag ctg tgg ctg gcc ctg cgg gca    1999
Gly Asp Phe Ala Gln Ala Ala Gln Gln Leu Trp Leu Ala Leu Arg Ala
                600                 605                 610
```

```
ctg ggc cgg ccc ctg ccc acc tcc cac ctg gac ctg gct tgt agc ctc     2047
Leu Gly Arg Pro Leu Pro Thr Ser His Leu Asp Leu Ala Cys Ser Leu
        615             620             625

ctc tgg aac ctc atc cgt cac ctg ctg cag cgt ctc tgg gtg ggc cgc     2095
Leu Trp Asn Leu Ile Arg His Leu Leu Gln Arg Leu Trp Val Gly Arg
        630             635             640

tgg ctg gca ggc cgg gca ggg ggc ctg cag cag gac tgt gct ctg cga     2143
Trp Leu Ala Gly Arg Ala Gly Gly Leu Gln Gln Asp Cys Ala Leu Arg
        645             650             655

gtg gat gct agc gcc agc gcc cga gac gca gcc ctg gtc tac cat aag     2191
Val Asp Ala Ser Ala Ser Ala Arg Asp Ala Ala Leu Val Tyr His Lys
660             665             670             675

ctg cac cag ctg cac acc atg ggg aag cac aca ggc ggg cac ctc act     2239
Leu His Gln Leu His Thr Met Gly Lys His Thr Gly Gly His Leu Thr
        680             685             690

gcc acc aac ctg gcg ctg agt gcc ctg aac ctg gca gag tgt gca ggg     2287
Ala Thr Asn Leu Ala Leu Ser Ala Leu Asn Leu Ala Glu Cys Ala Gly
        695             700             705

gat gcc gtg tct gtg gcg acg ctg gcc gag atc tat gtg gcg gct gca     2335
Asp Ala Val Ser Val Ala Thr Leu Ala Glu Ile Tyr Val Ala Ala Ala
        710             715             720

ttg aga gtg aag acc agt ctc cca cgg gcc ttg cat ttt ctg aca cgc     2383
Leu Arg Val Lys Thr Ser Leu Pro Arg Ala Leu His Phe Leu Thr Arg
        725             730             735

ttc ttc ctg agc agt gcc cgc cag gcc tgc ctg gca cag agt ggc tca     2431
Phe Phe Leu Ser Ser Ala Arg Gln Ala Cys Leu Ala Gln Ser Gly Ser
740             745             750             755

gtg cct cct gcc atg cag tgg ctc tgc cac ccc gtg ggc cac cgt ttc     2479
Val Pro Pro Ala Met Gln Trp Leu Cys His Pro Val Gly His Arg Phe
            760             765             770

ttc gtg gat ggg gac tgg tcc gtg ctc agt acc cca tgg gag agc ctg     2527
Phe Val Asp Gly Asp Trp Ser Val Leu Ser Thr Pro Trp Glu Ser Leu
            775             780             785

tac agc ttg gcc ggg aac cca gtg gac ccc ctg gcc cag gtg act cag     2575
Tyr Ser Leu Ala Gly Asn Pro Val Asp Pro Leu Ala Gln Val Thr Gln
        790             795             800

cta ttc cgg gaa cat ctc tta gag cga gca ctg aac tgt gtg acc cag     2623
Leu Phe Arg Glu His Leu Leu Glu Arg Ala Leu Asn Cys Val Thr Gln
        805             810             815

ccc aac ccc agc cct ggg tca gct gat ggg gac aag gaa ttc tcg gat     2671
Pro Asn Pro Ser Pro Gly Ser Ala Asp Gly Asp Lys Glu Phe Ser Asp
820             825             830             835

gcc ctc ggg tac ctg cag ctg ctg aac agc tgt tct gat gct gcg ggg     2719
Ala Leu Gly Tyr Leu Gln Leu Leu Asn Ser Cys Ser Asp Ala Ala Gly
            840             845             850

gct cct gcc tac agc ttc tcc atc agt tcc agc atg gcc acc acc acc     2767
Ala Pro Ala Tyr Ser Phe Ser Ile Ser Ser Ser Met Ala Thr Thr Thr
        855             860             865
```

```
ggc gta gac ccg gtg gcc aag tgg tgg gcc tct ctg aca gct gtg gtg    2815
Gly Val Asp Pro Val Ala Lys Trp Trp Ala Ser Leu Thr Ala Val Val
        870             875             880

atc cac tgg ctg cgg cgg gat gag gag gcg gct gag cgg ctg tgc ccg    2863
Ile His Trp Leu Arg Arg Asp Glu Glu Ala Ala Glu Arg Leu Cys Pro
        885             890             895

ctg gtg gag cac ctg ccc cgg gtg ctg cag gag tct gag aga ccc ctg    2911
Leu Val Glu His Leu Pro Arg Val Leu Gln Glu Ser Glu Arg Pro Leu
900             905             910             915

ccc agg gca gct ctg cac tcc ttc aag gct gcc cgg gcc ctg ctg ggc    2959
Pro Arg Ala Ala Leu His Ser Phe Lys Ala Ala Arg Ala Leu Leu Gly
            920             925             930

tgt gcc aag gca gag tct ggt cca gcc agc ctg acc atc tgt gag aag    3007
Cys Ala Lys Ala Glu Ser Gly Pro Ala Ser Leu Thr Ile Cys Glu Lys
            935             940             945

gcc agt ggg tac ctg cag gac agc ctg gct acc aca cca gcc agc agc    3055
Ala Ser Gly Tyr Leu Gln Asp Ser Leu Ala Thr Thr Pro Ala Ser Ser
            950             955             960

tcc att gac aag gcc gtg cag ctg ttc ctg tgt gac ctg ctt ctt gtg    3103
Ser Ile Asp Lys Ala Val Gln Leu Phe Leu Cys Asp Leu Leu Leu Val
        965             970             975

gtg cgc acc agc ctg tgg cgg cag cag cag ccc ccg gcc ccg gcc cca    3151
Val Arg Thr Ser Leu Trp Arg Gln Gln Gln Pro Pro Ala Pro Ala Pro
980             985             990             995

gca gcc cag ggc gcc agc agc agg ccc cag gct tcc gcc ctt gag ctg    3199
Ala Ala Gln Gly Ala Ser Ser Arg Pro Gln Ala Ser Ala Leu Glu Leu
            1000            1005            1010

cgt ggc ttc caa cgg gac ctg agc agc ctg agg cgg ctg gca cag agc    3247
Arg Gly Phe Gln Arg Asp Leu Ser Ser Leu Arg Arg Leu Ala Gln Ser
            1015            1020            1025

ttc cgg ccc gcc atg cgg agg gtg ttc cta cat gag gcc acg gcc cgg    3295
Phe Arg Pro Ala Met Arg Arg Val Phe Leu His Glu Ala Thr Ala Arg
        1030            1035            1040

ctg atg gcg ggg gcc agc ccc aca cgg aca cac cag ctc ctc gac cgc    3343
Leu Met Ala Gly Ala Ser Pro Thr Arg Thr His Gln Leu Leu Asp Arg
        1045            1050            1055

agt ctg agg cgg cgg gca ggc ccc ggt ggc aaa gga ggc gcg gtg gcg    3391
Ser Leu Arg Arg Arg Ala Gly Pro Gly Gly Lys Gly Gly Ala Val Ala
1060            1065            1070            1075

gag ctg gag ccg cgg ccc acg cgg cgg gag cac gcg gag gcc ttg ctg    3439
Glu Leu Glu Pro Arg Pro Thr Arg Arg Glu His Ala Glu Ala Leu Leu
            1080            1085            1090

ctg gcc tcc tgc tac ctg ccc ccc ggc ttc ctg tcg gcg ccc ggg cag    3487
Leu Ala Ser Cys Tyr Leu Pro Pro Gly Phe Leu Ser Ala Pro Gly Gln
        1095            1100            1105

cgc gtg ggc atg ctg gct gag gcg gcg cgc aca ctc gag aag ctt ggc    3535
Arg Val Gly Met Leu Ala Glu Ala Ala Arg Thr Leu Glu Lys Leu Gly
        1110            1115            1120
```

```
gat cgc cgg ctg ctg cac gac tgt cag cag atg ctc atg cgc ctg ggc       3583
Asp Arg Arg Leu Leu His Asp Cys Gln Gln Met Leu Met Arg Leu Gly
    1125              1130              1135

ggt ggg acc act gtc act tcc agc tag accccgtgtc cccggcctca            3630
Gly Gly Thr Thr Val Thr Ser Ser
1140              1145

gcacccctgt ctctagccac tttggtcccg tgcagcttct gtcctgcgtc gaagctttga   3690

aggccgaagg cagtgcaaga gactctggcc tccacagttc gacctgcggc tgctgtgtgc   3750

cttcgcggtg gaaggcccga ggggcgcgat cttgaccctga gaccggcgg ccatgatggt   3810

gctgacctct ggtggccgat cggggcactg caggggccga gccattttgg ggggcccccc   3870

tccttgctct gcaggcacct tagtggcttt tttcctcctg tgtacaggga agagaggggt   3930

acatttccct gtgctgacgg aagccaactt ggctttcccg gactgcaagc agggctctgc   3990

cccagaggcc tctctctccg tcgtgggaga gagacgtgta catagtgtag gtcagcgtgc   4050

ttagcctcct gacctgaggc tcctgtgcta ctttgccttt tgcaaacttt attttcatag   4110

attgagaagt tttgtacaga gaattaaaaa tgaaattatt tata                    4154
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<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 21
tgtctgcaca gtggtgccag                                                20


<210> 22
<211> 20
<212> DNA
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<220>

<223> Antisense Oligonucleotide

<400> 22
ctccgagtca ctgccactgc                                                20


<210> 23
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<220>

<223> Antisense Oligonucleotide

<400> 23
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tgaagcatgt cttcgaaagt   20

<210> 24
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<400> 24
gtcactgtct tggttgttga   20

<210> 25
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gggaagtcac tgtcttggtt   20

<210> 26
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<400> 26
ggccagggaa gtcactgtct   20

<210> 27
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<400> 27
gagtctgcct tgatgaagtg   20

<210> 28
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<400> 28
gccttgctgc cagctgcgag                                                    20


<210> 29
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<400> 29
gcagatttat tcagctttgc                                                    20


<210> 30
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<220>

<223> Antisense Oligonucleotide

<400> 30
agacagcaga tttattcagc                                                    20


<210> 31
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<213> Artificial Sequence

<220>

<223> Antisense Oligonucleotide

<400> 31
gcgcaagaca gcagatttat                                                    20


<210> 32
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<223> Antisense Oligonucleotide

<400> 32
gccttgcgca agacagcaga                                                    20


<210> 33
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<400> 33
cgatggcctt gcgcaagaca   20

<210> 34
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<400> 34
gtagtcgatg gccttgcgca   20

<210> 35
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<400> 35
aggcgggagc ggtccagcat   20

<210> 36
<211> 20
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<220>

<223> Antisense Oligonucleotide

<400> 36
ggcagagcca ctgcatggca   20

<210> 37
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<400> 37
gaggcccacc acttggccac   20

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gccagtggat caccacagct   20

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ccgggcagcc ttgaaggagt   20

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gcaggtaccc actggccttc   20

<210> 42
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<220>

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<400> 42
ctatgaaaat aaagtttgca   20

<210> 43
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<400> 43
gccgacttca cctgtcaagg   20

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

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cttcctcaga ctgtaggcaa atcttgctgc tgccattcga tgcgaagggc caggagtggg   180

taaactgagg ctaaaatggt ccaggcaagt tctgggtgtg tgcgaacgaa ccagcggtgg   240

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gcagcccagg tgccaactct cctgagagct ctcttctgc ttctctggcc tcctctctgg   240

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aagccttcct gggaggaccc aaggtgacac ctgcaccctt gtcccctcca ccatcggcac    300

ccgctgcttt aaagatgtac ccgtccgtgt ccccctttttc ccctgggcct gngatcaaag    360

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